

SEQUENCE LISTING

<110> PUBLIC UNIVERSITY OF NAVARRA
<120> "Plant nucleotide sugar
5 pyrophosphatase/phosphodiesterase (NPPase), method of
production, use in the manufacture of testing devices
and in the production of transgenic plants"

<130>
<160>
<210> 1
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<212> Peptide
<213> Hordeum vulgare cv. Scarlett
<220>
<223> N-terminal end of soluble NPPase
<400>
Ala Ala Val Arg Ala Ser Pro Asp Leu Leu Gly Ser Arg Gly Glu
5 10 15
Asp
<210> 2
<211> 11
<212> Peptide
<213> Hordeum vulgare cv. Scarlett
<220>
<223> Tryptic sequence of soluble NPPase
<220> Variant
<222> 6
<223> / Nota = Lys
<220> Variant
<222> 9
<223> / Nota = Ile

<220> Variant

<222> 10

<223> / Nota = Lys

<400>

Ala Ser Tyr Pro Gly Gln Thr Ser Leu Gln Arg

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10

<210> 3

<211> 11

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<220> Variant

<222> 9

<223> / Nota = Met

<400>

His Ala Pro Ala Asp Thr Val Thr Phe Gly Arg

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10

<210> 4

<211> 5

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<400>

Ala Pro Pro Tyr Pro

5

<210> 5

<211> 8

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<400>

Ala Trp Val Thr Val Glu Phe Lys

5

<210> 6

<211> 8

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<220> Variant

<222> 1

<223> / Nota = Lys

<220> Variant

<222> 3

<223> / Nota = Ile

<220> Variant

<222> 6

<223> / Nota = Ile

<400>

Gln Ser Leu Glu Gly Leu Trp Arg

5

<210> 7

<211> 15

<212> Peptide

<213> Oryza sativa

<220>

<223> N-terminal end of soluble NPPase

<400>

Gly Ser Ala Phe Val Ser Ala Thr Pro Ala Leu Leu Gly Asp Gln

5

10

15

<210> 8

<211> 23

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Phe Gln Leu Leu Asn Gln Arg Tyr Asp Phe Ser Phe Ala Leu Glu

5

10

15

Thr Gly Gly Leu Glu Asn Pro Lys

20

<210> 9

<211> 11

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Leu Val Ala Val Ser Glu Ala Leu Ser Phe Lys
5 10

<210> 10

<211> 10

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (Edman) of soluble NPPase

<400>

Leu Ala Gln Gly Lys Ser Tyr Asp Glu Met
5 10

<210> 11

<211> 10

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Thr Ala Ala Gly Thr Leu Thr Phe Asn Arg
5 10

<210> 12

<211> 11

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Asp Pro Gly Phe Leu His Thr Ala Phe Leu Arg
5 10

<210> 13

<211> 12

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Ala Pro Asp Phe Pro Gly Gln Asn Ser Leu Gln Arg
5 10

<210> 14

<211> 9

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Ile Ile Val Phe Gly Asp Met Gly Lys
5

<210> 15

<211> 12

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Asp Trp Pro Asn Thr Gly Gly Phe Phe Asp Val Lys
5 10

<210> 16

<211> 11

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Phe Ile Glu Gln Cys Leu Ser Thr Val Asp Arg
5 10

<210> 17

<211> 9

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Val Tyr Asp Ser Phe Tyr Val Glu Arg
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<210> 18

<211> 18

<212> ADN

<213> Oryza sativa

<220>

<223> Primer of the 5' region of NPPase

<400>

ggcgttgctc ggcgacca

<210> 19

<211> 19

<212> ADN

<213> Oryza sativa

<220>

<223> Primer of the 3' region of NPPase

<400>

gaggcgagcg tggtgaaaa

<210> 20

<211> 2186

<212> ADN

<213> Oryza sativa

<220>

<223> complete cDNA of rice NPPase

<400>

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ggc	gtg	gca	atg	gct	gtg	gct	atg	ctg	ctg	90
gct	cg	tcg	tcg	120						
tcg	ctg	gaa	ggg	ttc	cag	ccg	ctg	tcg	aag	150
atc	gcc	gtc	cac	aag	gcc	acc	gtc	gac	ctc	180
cac	ggc	tcc	gct	ttc	gtc	agc	gcc	acg	ccg	210
gct	ttg	ctc	ggc	gac	cag	gga	gaa	gac	aca	240
gag	tgg	gtc	acg	gtg	aaa	tac	ggc	tgg	gca	270
aac	cct	tcc	gct	gac	gac	tgg	att	gtc	gtc	300
ttc	tct	ccg	gcc	gat	ttc	atc	tcg	gg	tct	330
tgc	cct	aat	cct	tcc	aga	tac	ccg	gat	gag	360
ccg	ctg	ctc	tgc	act	gca	cca	ata	aag	tat	390
caa	tcc	gca	aac	tac	tcg	gct	aac	tac	gtg	420
tac	tgg	ggc	aag	ggc	agc	atc	ccg	ttc	cag	450
ctc	atc	aat	cag	cgc	tac	gac	ttc	tcc	ttc	480
gcc	ctg	tcc	acc	ggc	ggc	ctg	gaa	aac	cct	510

aag ctg gtg gcg gtg tcg gag ggc ata tcg 540
 ttc aag aac ccc aag gcg ccg gtg tac cct 570
 cgg ctg gcg cag ggc aag tcg tac gac gag 600
 atg acc gtc aca tgg acc agc ggc tac gac 630
 atc agc gag ggc tac ccg ttc gtc gag tgg 660
 ggc atg gtc gtc gcc ggc gcc gcc gct cca 690
 acc cgc acc gcc gcc ggc acg ctc acc ttc 720
 aac cgc ggc agc atg tgc ggt gac ccg gac 750
 cgc act gtt ggg tgg aga gac ccc ggg ttc 780
 atc cac aca gct ttc ctg aga gac ctg tgg 810
 ccc aac aaa gag tac tac tac aag att ggg 840
 cat gaa ctt tct gac gga tca att gtc tgg 870
 ggc aag caa tac act ttc cgg ggc cca ccc 900
 ttc cct ggc cag aac tcg ctg caa cgc atc 930
 atc gtc ttc ggc gac atg ggc aag gcg gag 960
 aga gac gga tca aac gag ttc gcc aac tac 990
 cag cca gga tct ctg aac acg acg gac agg 1020
 ctg gtc gag gat ctg gac aac tac gac att 1050
 gtc ttc cac atc ggt gat ctt cgg tac gcc 1080
 aat ggc tac atc tcc cag tgg gac cag ttc 1110
 acc gcc cag gtc gcc ccc atc acc gcc aag 1140
 aag ccc tac atg att gca agc ggt aac cat 1170
 gag agg gac tgg ccc aac acc gga ggg ttc 1200
 ttc gac gtc aag gac tcc ggc ggc gag tgc 1230
 ggc gtt ccg gca gag acc atg tac tac tac 1260
 ccg gcc gag aat cga gcc aac ttc tgg tac 1290
 aag gtg gac tac ggg atg ttc cgg ttc tgc 1320
 atc gcg gac tcg gag cac gac tgg agg gag 1350
 ggt acc gac cag tac aag ttc atc gag cag 1380
 tgc ctg tcg acg gtg gac cgg aag cac cag 1410
 ccg tgg ctc atc ttc gcg gcg cac cgc gtg 1440
 ctg ggc tac tcc tcc aac tgg tgg tac gcc 1470
 gac cag ggc tcc ttc gag gag ccc gaa ggg 1500
 agg gag agc ctg cag cgg ctg tgg cag cgc 1530
 cac cgc gtc gac gtc gcc ttc ttc ggc cac 1560
 gtc cac aac tac gag cgg acg tgc cgg atg 1590
 tac cag agc cag tgc gtc tcc ggc gag agg 1620
 cgc cgc tac tcc ggc acc atg aac ggc acc 1650
 atc ttc gtc gtc gcc ggc ggc ggg agc 1680
 cac ctc tcg gac tac acc tcg gcg atc ccc 1710
 aag tgg agc gtt ttc agg gac cgg gac ttc 1740
 ggg ttc gtc aag ctc acc gcg ttc aac cac 1770
 tcg tcg ctg ctg ttc gag tac aag aag agc 1800
 agc gat ggg aag gtg tat gac tcc ttc acc 1830
 gtg gag agg gat tac cgc gac gtg ctc agc 1860
 tgc gtg cac gac agc tgc ctc ccc acc acg 1890
 ctc gcc tcc tga tga atg aaa caa ggg aaa 1920
 gga tca tta tta gga tgc atg agt tga tgc 1950

ctc atc gtc aaa atg ctg gca gct gag aaa 1980
 gag tga tcg gtc ggt cga tcg agt tgg gtt 2010
 tta ttt ttt ttc ttc ttc aac cat ttc 2040
 gat cag gtg tgg tag tgg tcg atc gct tgg 2070
 ctc gat cgt gtt tct ctt cct cat gga tgg 2100
 tga tgt tgt gca ata aaa ttg ctt agc tgc 2130
 tcg ggc aca aat gtc taa aaa aaa aaa aaa 2160
 aaa aaa aaa aaa aaa aaa aaa aa 2186

<210> 21

<211> 623

<212> Peptide

<213> Oryza sativa

<220>

<223> Amino acid sequence of rice NPPase

<400>

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									25	30		35					40		
Ile	Ala	Val	His	Lys	Ala	Thr	Val	Asp	Leu	His	Gly	Ser	Ala	Phe	Val	Ser	Ala	Thr	Pro
								45	50		55					60			
Ala	Leu	Leu	Gly	Asp	Gln	Gly	Glu	Asp	Thr	Glu	Trp	Val	Thr	Val	Lys	Tyr	Gly	Trp	Ala
					65	70		75								80			
Asn	Pro	Ser	Ala	Asp	Asp	Trp	Ile	Ala	Val	Phe	Ser	Pro	Ala	Asp	Phe	Ile	Ser	Gly	Ser
					85	90		95								100			
Cys	Pro	Asn	Pro	Ser	Arg	Tyr	Pro	Asp	Glu	Pro	Leu	Leu	Cys	Thr	Ala	Pro	Ile	Lys	Tyr
					105	110		115								120			
Gln	Phe	Ala	Asn	Tyr	Ser	Ala	Asn	Tyr	Val	Tyr	Trp	Gly	Lys	Gly	Ser	Ile	Arg	Phe	Gln
					125	130		135								140			
Leu	Ile	Asn	Gln	Arg	Tyr	Asp	Phe	Ser	Phe	Ala	Leu	Phe	Thr	Gly	Gly	Leu	Asn	Pro	
					145	150		155								160			
Lys	Leu	Val	Ala	Val	Ser	Glu	Ala	Ile	Ser	Phe	Lys	Asn	Pro	Lys	Ala	Pro	Val	Tyr	Pro
					165	170		175								180			
Arg	Leu	Ala	Gln	Gly	Lys	Ser	Tyr	Asp	Glu	Met	Thr	Val	Thr	Trp	Thr	Ser	Gly	Tyr	Asp
					185	190		195								200			
Ile	Ser	Glu	Ala	Tyr	Pro	Phe	Val	Glu	Trp	Gly	Met	Val	Val	Ala	Gly	Ala	Ala	Pro	
					205	210		215								220			
Thr	Arg	Thr	Ala	Ala	Gly	Thr	Leu	Thr	Phe	Asn	Arg	Gly	Ser	Met	Cys	Gly	Asp	Pro	Asp
					225	230		235								240			
Arg	Thr	Val	Gly	Trp	Arg	Asp	Pro	Gly	Phe	Ile	His	Thr	Ala	Phe	Leu	Arg	Asp	Leu	Trp
					245	250		255								260			
Pro	Asn	Lys	Glu	Tyr	Tyr	Tyr	Lys	Ile	Gly	His	Glu	Leu	Ser	Asp	Gly	Ser	Ile	Val	Trp
					265	270		275								280			
Gly	Lys	Gln	Tyr	Thr	Phe	Arg	Ala	Pro	Pro	Phe	Gly	Gln	Asn	Ser	Leu	Gln	Arg	Ile	
					285	290		295								300			
Ile	Val	Phe	Gly	Asp	Met	Gly	Lys	Ala	Glu	Arg	Asp	Gly	Ser	Asn	Glu	Phe	Ala	Asn	Tyr
					305	310		315								320			
Gln	Pro	Gly	Ser	Leu	Asn	Thr	Thr	Asp	Arg	Leu	Val	Glu	Asp	Leu	Asp	Asn	Tyr	Asp	Ile
					325	330		335								340			

Val Phe His Ile Gly Asp Leu Pro Tyr Ala Asn Gly Tyr Ile Ser Gln Trp Asp Gln Phe
 345 350 355 360
 Thr Ala Gln Val Ala Pro Ile Thr Ala Lys Lys Pro Tyr Met Ile Ala Ser Gly Asn His
 365 370 375 380
 Glu Arg Asp Trp Pro Asn Thr Gly Gly Phe Phe Asp Val Lys Asp Ser Gly Gly Glu Cys
 385 390 395 400
 Gly Val Pro Ala Glu Thr Met Tyr Tyr Pro Ala Glu Asn Arg Ala Asn Phe Trp Tyr
 405 410 415 420
 Lys Val Asp Tyr Gly Met Phe Arg Phe Cys Ile Ala Asp Ser Glu His Asp Trp Arg Glu
 425 430 435 440
 Gly Thr Asp Gln Tyr Lys Phe Ile Glu Gln Cys Leu Ser Thr Val Asp Arg Lys His Gln
 445 450 455 460
 Pro Trp Leu Ile Phe Ala Ala His Arg Val Leu Gly Tyr Ser Ser Asn Trp Trp Tyr Ala
 465 470 475 480
 Asp Gln Gly Ser Phe Glu Glu Pro Glu Gly Arg Glu Ser Leu Gln Arg Leu Trp Gln Arg
 485 490 495 500
 His Arg Val Asp Val Ala Phe Phe Gly His Val His Asn Tyr Glu Arg Thr Cys Pro Met
 505 510 515 520
 Tyr Gln Ser Gln Cys Val Ser Gly Glu Arg Arg Arg Tyr Ser Gly Thr Met Asn Gly Thr
 525 530 535 540
 Ile Phe Val Val Ala Gly Gly Gly Ser His Leu Ser Asp Tyr Thr Ser Ala Ile Pro
 545 550 555 560
 Lys Trp Ser Val Phe Arg Asp Arg Asp Phe Gly Phe Val Lys Leu Thr Ala Phe Asn His
 565 570 575 580
 Ser Ser Leu Leu Phe Glu Tyr Lys Lys Ser Ser Asp Gly Lys Val Tyr Asp Ser Phe Thr
 585 590 595 600
 Val Glu Arg Asp Tyr Arg Asp Val Leu Ser Cys Val His Asp Ser Cys Leu Pro Thr Thr
 605 610 615 620
 Leu Ala Ser

<210> 22

<211> 1268

<212> ADN

<213> Hordeum vulgare cv. Scarlett

<220>

<223> incomplete cDNA of barley NPPase

<400>

ctc	cga	cgg	aag	cgt	ggt	gtg	ggc	caa	gcc	30
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gca	gaa	ctc	gct	gca	gcg	tat	cat	cgt	ctt	90
cg	tg	ca	t	gg	aa	gg	gg	ga	cg	120
atc	aaa	cga	gtt	cgc	caa	cta	cca	gcc	gg	150
gtc	gct	caa	cac	gac	gga	cag	gct	gat	tga	180
aga	tct	gga	caa	cta	cga	cat	cgt	ctt	cca	210
cat	cgg	cga	cat	gcc	cta	cgc	caa	cgg	gta	240
cct	ctc	cca	gtg	gga	cca	gtt	cac	cgc	aca	270
ggt	cgc	ccc	cat	cag	cgc	caa	gaa	acc	cta	300
cat	ggt	tgc	aag	cgg	caa	cca	cga	gag	gga	330
ctg	gcc	caa	cac	cgg	gtt	ctt	cga	cgt		360

caa gga ctc cgg cgg cga atg cgg cgt gcc	390
ggc cga gac cat gta cta cta ccc cgc cga	420
aaa cag ggc aaa ctt ctg gta caa ggt gga	450
cta cgg gat gtt ccg gtt ctg cgt ggg gga	480
ctc gga gca cga ctg gag gga ggg cac ccc	510
gca gta caa gtt cat cga gga gtg cct gtc	540
gac ggt gga ccg gaa gca cca gcc gtg gct	570
cat ctt cac ggc gca ccg ggt gct ggg cta	600
ctc ctc caa ctc gtg gta cgc cga cca ggg	630
ctc ctt cga gga gcc cga ggg acg gga gag	660
cct gca gaa gct gtg gca gcg cta ccg cgt	690
cga cat cgc ctc ctt ccg cca cgt cca caa	720
cta cga gcg cac atg ccc gct cta cca gag	750
cca gtg cgt caa cgc cga caa gac cca cta	780
ctc ggg cac cat gaa ccg cac cat ctt cgt	810
cgt cgc ccg ccg ggg ccg cag cca cct gtc	840
gtc cta cac cac cgc cat ccc caa gtg gag	870
cat att cag gga cca tga cta ccg gtt cac	900
caa gct cac cgc att caa cca ctc ctc gct	930
tct ctt cga gta cat gaa gag cag cga ccg	960
caa ggt cta cga ctc ctt cac cat cca cag	990
gga tta ccg cga cgt gct cag ctg cgt gca	1020
cga cag ctg ctt ccc cac cac gct cgc tag	1050
cta gct cat atc gtc ccg ccg tca tgt caa	1080
tgt aat gga ggg tca tcc atc caa taa aat	1110
tgt ggg cat gtg ttg agt aat aaa att ggt	1140
cag ctg cac aat tta tat gtg cta gta aaa	1170
aga tca tgc aag agg tgg gtg tat gct cgt	1200
tat ata tgc ttt gta act cct tca tgt cat	1230
att att atg ggt taa taa aaa cat cct tta	1260
tta aaa aa	1268

<210> 23

<211> 350

<212> Peptide

<213> *Hordeum vulgare* cv. Scarlett

<220>

<223> Amino acid sequence deduced from the cDNA of barley NPPase

<400>

Ser Asp Gly Ser Val Val Trp Ala Lys Pro Tyr Thr Phe Arg Ala Pro Pro Pro Thr Pro Gly
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 Gln Asn Ser Leu Gln Arg Ile Ile Val Phe Gly Asp Met Gly Lys Ala Glu Arg Asp Gly
 25 30 35 40
 Ser Asn Glu Phe Ala Asn Tyr Gin Pro Gly Ser Leu Asn Thr Thr Asp Arg Leu Ile Glu
 45 50 55 60
 Asp Leu Asp Asn Tyr Asp Ile Val Phe His Ile Gly Asp Met Pro Tyr Ala Asn Gly Tyr
 65 70 75 80
 Leu Ser Gln Trp Asp Gln Phe Thr Ala Gln Val Ala Pro Ile Ser Ala Lys Lys Pro Tyr
 85 90 95 100
 Met Val Ala Ser Gly Asn His Glu Arg Asp Trp Pro Asn Thr Gly Gly Phe Phe Asp Val
 105 110 115 120
 Lys Asp Ser Gly Gly Glu Cys Gly Val Pro Ala Glu Thr Met Tyr Tyr Tyr Pro Ala Glu
 125 130 135 140
 Asn Arg Ala Asn Phe Trp Tyr Lys Val Asp Tyr Gly Met Phe Arg Phe Cys Val Gly Asp
 145 150 155 160
 Ser Glu His Asp Trp Arg Glu Gly Thr Pro Gln Tyr Lys Phe Ile Glu Glu Cys Leu Ser
 165 170 175 180
 Thr Val Asp Arg Lys His Gln Pro Trp Leu Ile Phe Thr Ala His Arg Val Leu Gly Tyr
 185 190 195 200
 Ser Ser Asn Ser Trp Tyr Ala Asp Gln Gly Ser Phe Glu Glu Pro Glu Gly Arg Glu Ser
 205 210 215 220
 Leu Gln Lys Leu Trp Gln Arg Tyr Arg Val Asp Ile Ala Ser Phe Gly His Val His Asn
 225 230 235 240
 Tyr Glu Arg Thr Cys Pro Leu Tyr Gln Ser Gln Cys Val Asn Ala Asp Lys Thr His Tyr
 245 250 255 260
 Ser Gly Thr Met Asn Gly Thr Ile Phe Val Val Ala Gly Gly Gly Ser His Leu Ser
 265 270 275 280
 Ser Tyr Thr Thr Ala Ile Pro Lys Trp Ser Ile Phe Arg Asp His Asp Tyr Gly Phe Thr
 285 290 295 300
 Lys Leu Thr Ala Phe Asn His Ser Ser Leu Leu Phe Glu Tyr Met Lys Ser Ser Asp Gly
 305 310 315 320
 Lys Val Tyr Asp Ser Phe Thr Ile His Arg Asp Tyr Arg Asp Val Leu Ser Cys Val His
 325 330 335 340
 Asp Ser Cys Phe Pro Thr Thr Leu Ala Ser
 345 350

<210> 24

<211> 39

<212> ADN

<213> *Hordeum vulgare* cv. *Scarlett*

<220>

<223> Primer of the 5' region of NPPase

soluble

<400>

gcagcagtac gagcatcacc agatctacta gcatcacga

39